

SEQUENCE LISTING

SEQ ID NO.1

SEQUENCE LENGTH: 556

SEQUENCE TYPE: amino acid

STRANNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION

Met Pro Ile Arg Leu Ser Lys Glu Lys Ile Asn Asp Leu Leu Gln Arg
1 5 10 15
Ser Gln Gly Asp Leu Thr Ser Ser Gln His Glu Ile Val His Phe Thr
20 25 30
Asp Val Phe Ile Ala Gly Ser Gly Pro Ile Ser Cys Thr Tyr Ala Arg
35 40 45
His Ile Ile Asp Asn Thr Ser Thr Lys Val Tyr Met Ala Glu Ile
50 55 60
Gly Ser Gln Asp Asn Pro Val Ile Gly Ala His His Lys Asn Ser Ile
65 70 75 80
Lys Phe Gln Lys Asp Ile Asp Lys Phe Val Asn Ile Ile Asn Gly Ala
85 90 95
Leu Gln Pro Ile Ser Ile Ser Pro Ser Asp Thr Tyr Gln Pro Thr Leu
100 105 110
Ala Val Ala Ala Trp Ala Pro Pro Ile Asp Pro Ala Glu Gly Gln Leu
115 120 125
Val Ile Met Gly His Asn Pro Asn Gln Glu Ala Gly Leu Asn Leu Pro
130 135 140
Gly Ser Ala Val Thr Arg Thr Val Gly Gly Met Ala Thr His Trp Thr
145 150 155 160
Cys Ala Cys Pro Thr Pro His Asp Glu Glu Arg Val Asn Asn Pro Val
165 170 175
Asp Lys Gln Glu Phe Asp Ala Leu Leu Glu Arg Ala Lys Thr Leu Leu
180 185 190
Asn Val His Ser Asp Gln Tyr Asp Asp Ser Ile Arg Gln Ile Val Val
195 200 205
Lys Glu Thr Leu Gln Gln Thr Leu Asp Ala Ser Arg Gly Val Thr Thr
210 215 220

Leu	Pro	Leu	Gly	Val	Glu	Arg	Arg	Thr	Asp	Asn	Pro	Ile	Tyr	Val	Thr
225				230					235					240	
Trp	Thr	Gly	Ala	Asp	Thr	Val	Leu	Gly	Asp	Val	Pro	Lys	Ser	Pro	Arg
				245					250					255	
Phe	Ala	Leu	Val	Thr	Glu	Thr	Arg	Val	Thr	Lys	Leu	Ile	Val	Ser	Glu
				260				265					270		
Thr	Asn	Pro	Thr	Gln	Val	Val	Ala	Ala	Leu	Leu	Arg	Asn	Leu	Asn	Thr
					275			280					285		
Ser	Asn	Asp	Glu	Leu	Val	Val	Ala	Lys	Ser	Phe	Val	Ile	Ala	Cys	Gly
				290			295			300					
Ala	Val	Cys	Thr	Pro	Gln	Ile	Leu	Trp	Asn	Ser	Asn	Ile	Arg	Pro	Tyr
305					310				315					320	
Ala	Leu	Gly	Arg	Tyr	Leu	Ser	Glu	Gln	Ser	Met	Thr	Phe	Cys	Gln	Ile
					325				330					335	
Val	Leu	Lys	Arg	Gly	Ile	Val	Asp	Ala	Ile	Ala	Thr	Asp	Pro	Arg	Phe
					340			345					350		
Ala	Ala	Lys	Val	Glu	Ala	His	Lys	Lys	Lys	His	Pro	Asp	Asp	Val	Leu
					355			360					365		
Pro	Ile	Pro	Phe	His	Glu	Pro	Glu	Pro	Gln	Val	Met	Ile	Pro	Tyr	Thr
					370			375			380				
Ser	Asp	Phe	Pro	Trp	His	Val	Gln	Val	His	Arg	Asp	Ala	Phe	Ser	Tyr
385						390			395					400	
Gly	Asp	Val	Gly	Pro	Lys	Ala	Asp	Pro	Arg	Val	Val	Val	Asp	Leu	Arg
						405			410					415	
Phe	Phe	Gly	Lys	Ser	Asp	Ile	Val	Glu	Glu	Asn	Arg	Val	Thr	Phe	Gly
						420			425					430	
Pro	Asn	Pro	Lys	Leu	Arg	Glu	Trp	Glu	Ala	Gly	Val	Thr	Asp	Thr	Tyr
						435			440					445	
Gly	Met	Pro	Gln	Pro	Thr	Phe	His	Val	Lys	Arg	Thr	Asn	Ala	Asp	Gly
						450			455			460			
Asp	Arg	Asp	Gln	Arg	Met	Met	Asn	Asp	Met	Thr	Asn	Val	Ala	Asn	Met
465								470			475			480	
Leu	Gly	Gly	Tyr	Leu	Pro	Gly	Ser	Tyr	Pro	Gln	Phe	Met	Ala	Pro	Gly
								485			490			495	
Leu	Val	Leu	His	Ile	Thr	Gly	Thr	Thr	Arg	Ile	Gly	Thr	Asp	Asp	Gln
						500			505					510	

Thr Ser Val Ala Asp Pro Thr Ser Lys Val His Asn Phe Asn Asn Leu			
515	520	525	
Trp Val Gly Gly Asn Gly Cys Ile Pro Asp Ala Thr Ala Cys Asn Pro			
530	535	540	
Thr Arg Thr Ser Val Ala Tyr Ala Leu Lys Gly Ala Glu Ala Val Val			
545	550	555	560
Asn Tyr Leu Gly Val Ser *			
	565		

SEQ ID NO.2

SEQUENCE LENGTH: 1701

SEQUENCE TYPE: nucleic acid

STRANDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA to RNA

SEQUENCE DESCRIPTION

ATG CCG ATA CGT CTT TCC AAA GAA AAA ATC AAC GAC CTG CTG CAA CGT	48
Met Pro Ile Arg Leu Ser Lys Glu Lys Ile Asn Asp Leu Leu Gln Arg	
1 5 10 15	
TCT CAA GGG GAT CTT ACT TCC TCG CAA CAC GAA ATT GTA CAT TTC ACT	96
Ser Gln Gly Asp Leu Thr Ser Ser Gln His Glu Ile Val His Phe Thr	
20 25 30	
GAT GTT TTC ATT GCT GGC AGT GGT CCC ATT AGC TGT ACT TAC GCC CGC	144
Asp Val Phe Ile Ala Gly Ser Gly Pro Ile Ser Cys Thr Tyr Ala Arg	
35 40 45	
CAC ATC ATT GAC AAT ACC TCA ACT ACA AAG GTT TAC ATG GCC GAA ATA	192
His Ile Ile Asp Asn Thr Ser Thr Thr Lys Val Tyr Met Ala Glu Ile	
50 55 60	
GGT TCT CAA GAT AAC CCT GTC ATC GGG GCC CAT CAC AAG AAC TCC ATA	240
Gly Ser Gln Asp Asn Pro Val Ile Gly Ala His His Lys Asn Ser Ile	
65 70 75 80	
AAG TTT CAG AAA GAC ATT GAC AAG TTT GTG AAT ATC ATC AAC GGT GCC	288
Lys Phe Gln Lys Asp Ile Asp Lys Phe Val Asn Ile Ile Asn Gly Ala	
85 90 95	

CTC CAG CCG ATT TCG ATT TCG CCA TCG GAC ACC TAC CAG CCC ACT CTC	336
Leu Gln Pro Ile Ser Ile Ser Pro Ser Asp Thr Tyr Gln Pro Thr Leu	
100 105 110	
GCT GTA GCA GCG TGG GCG CCG CCC ATC GAT CCT GCC GAA GGC CAG CTC	384
Ala Val Ala Ala Trp Ala Pro Pro Ile Asp Pro Ala Glu Gly Gln Leu	
115 120 125	
GTG ATT ATG GGA CAC AAT CCG AAT CAG GAG GCC GGC CTG AAC CTT CCC	432
Val Ile Met Gly His Asn Pro Asn Gln Glu Ala Gly Leu Asn Leu Pro	
130 135 140	
GGT AGC GCT GTC ACT AGG ACA GTC GGG GGG ATG GCG ACC CAC TGG ACT	480
Gly Ser Ala Val Thr Arg Thr Val Gly Gly Met Ala Thr His Trp Thr	
145 150 155 160	
TGC GCG TGT CCT ACT CCA CAT GAC GAA GAG AGG GTC AAC AAC CCA GTT	528
Cys Ala Cys Pro Thr Pro His Asp Glu Glu Arg Val Asn Asn Pro Val	
165 170 175	
GAC AAG CAG GAG TTC GAC GCA CTG CTC GAA CGT GCT AAA ACA TTG CTC	576
Asp Lys Gln Glu Phe Asp Ala Leu Leu Glu Arg Ala Lys Thr Leu Leu	
180 185 190	
AAC GTT CAC AGC GAC CAG TAC GAC GAT TCT ATC CGT CAG ATA GTT GTC	624
Asn Val His Ser Asp Gln Tyr Asp Asp Ser Ile Arg Gln Ile Val Val	
195 200 205	
AAA GAG ACT CTT CAG CAG ACC CTT GAT GCG TCG CGG GGT GTG ACC ACT	672
Lys Glu Thr Leu Gln Gln Thr Leu Asp Ala Ser Arg Gly Val Thr Thr	
210 215 220	
CTC CCG CTG GGG GTG GAG CGC CGT ACG GAC AAT CCT ATT TAT GTC ACC	720
Leu Pro Leu Gly Val Glu Arg Arg Thr Asp Asn Pro Ile Tyr Val Thr	
225 230 235 240	
TGG ACC GGT GCC GAT ACC GTC CTT GGT GAT GTG CCG AAG AGT CCC CGA	768
Trp Thr Gly Ala Asp Thr Val Leu Gly Asp Val Pro Lys Ser Pro Arg	
245 250 255	
TTC GCT TTG GTT ACA GAG ACG AGA GTG ACG AAG CTT ATT GTC AGT GAA	816
Phe Ala Leu Val Thr Glu Thr Arg Val Thr Lys Leu Ile Val Ser Glu	
260 265 270	
ACC AAT CCG ACG CAG GTT GTC GCG TTG CTA CGT AAC TTG AAT ACA	864
Thr Asn Pro Thr Gln Val Val Ala Ala Leu Leu Arg Asn Leu Asn Thr	
275 280 285	

AGC AAC GAT GAA CTT GTC GTG GCC AAG AGT TTC GTC ATA GCT TGT GGA	912
Ser Asn Asp Glu Leu Val Val Ala Lys Ser Phe Val Ile Ala Cys Gly	
290 295 300	
GCA GTC TGC ACA CCG CAA ATC TTG TGG AAC AGC AAC ATC CGC CCA TAT	960
Ala Val Cys Thr Pro Gln Ile Leu Trp Asn Ser Asn Ile Arg Pro Tyr	
305 310 315 320	
GCG CTT GGT CGC TAC CTC AGC GAA CAG TCC ATG ACT TTT TGT CAG ATC	1008
Ala Leu Gly Arg Tyr Leu Ser Glu Gln Ser Met Thr Phe Cys Gln Ile	
325 330 335	
GTT CTC AAG AGG GGC ATA GTC GAT GCC ATC GCT ACT GAC CCT CGC TTC	1056
Val Leu Lys Arg Gly Ile Val Asp Ala Ile Ala Thr Asp Pro Arg Phe	
340 345 350	
GCG AAG GTT GAG GCG CAC AAG AAG CAC CCC GAT GAC GTG CTG	1104
Ala Ala Lys Val Glu Ala His Lys Lys His Pro Asp Asp Val Leu	
355 360 365	
CCC ATT CCA TTC CAC GAG CCT GAA CCT CAA GTG ATG ATT CCG TAC ACG	1152
Pro Ile Pro Phe His Glu Pro Glu Pro Gln Val Met Ile Pro Tyr Thr	
370 375 380	
TCG GAC TTC CCT TGG CAT GTT CAG GTG CAT CGC GAT GCA TTC TCA TAT	1200
Ser Asp Phe Pro Trp His Val Gln Val His Arg Asp Ala Phe Ser Tyr	
385 390 395 400	
GGT GAT GTT GGA CCC AAG GCC GAC CCG CGT GTT GTC GTC GAT CTG AGG	1248
Gly Asp Val Gly Pro Lys Ala Asp Pro Arg Val Val Val Asp Leu Arg	
405 410 415	
TTT TTC GGC AAA TCA GAT ATT GTC GAA GAA AAT CGA GTG ACT TTC GGT	1296
Phe Phe Gly Lys Ser Asp Ile Val Glu Glu Asn Arg Val Thr Phe Gly	
420 425 430	
CCG AAC CCT AAG CTA CGC GAG TGG GAA GCG GGT GTT ACA GAC ACT TAT	1344
Pro Asn Pro Lys Leu Arg Glu Trp Glu Ala Gly Val Thr Asp Thr Tyr	
435 440 445	
GGA ATG CCA CAG CCG ACA TTC CAT GTC AAG CGG ACC AAC GCC GAT GGA	1392
Gly Met Pro Gln Pro Thr Phe His Val Lys Arg Thr Asn Ala Asp Gly	
450 455 460	
GAC CGT GAC CAG AGG ATG ATG AAT GAT ATG ACC AAC GTC GCG AAC ATG	1440
Asp Arg Asp Gln Arg Met Met Asn Asp Met Thr Asn Val Ala Asn Met	
465 470 475 480	

CTG GGT GGG TAC CTT CCT GGC TCC TAC CCT CAA TTT ATG GCA CCT GGT	1488		
Leu Gly Gly Tyr Leu Pro Gly Ser Tyr Pro Gln Phe Met Ala Pro Gly			
485	490	495	
CTC GTA CTG CAC ATC ACG GGA ACT ACT CGG ATC GGG ACA GAT GAT CAA	1536		
Leu Val Leu His Ile Thr Gly Thr Thr Arg Ile Gly Thr Asp Asp Gln			
500	505	510	
ACT TCT GTT GCT GAT CCG ACA TCA AAG GTT CAT AAC TTC AAC AAT CTG	1584		
Thr Ser Val Ala Asp Pro Thr Ser Lys Val His Asn Phe Asn Asn Leu			
515	520	525	
TGG GTC GGC GGG AAT GGG TGC ATT CCA GAT GCG ACT GCC TGC AAC CCG	1632		
Trp Val Gly Gly Asn Gly Cys Ile Pro Asp Ala Thr Ala Cys Asn Pro			
530	535	540	
ACT CGT ACG AGC GTC GCG TAT GCG CTC AAG GGT GCT GAG GCT GTA GTC	1680		
Thr Arg Thr Ser Val Ala Tyr Ala Leu Lys Gly Ala Glu Ala Val Val			
545	550	555	560
AAT TAC CTT GGC GTC TCC TGA	1701		
Asn Tyr Leu Gly Val Ser *			
565			

SEQ ID NO.3

SEQUENCE LENGTH: 29

SEQUENCE TYPE: amino acid

STRANDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION

Pro Ile Arg Leu Ser Lys Glu Lys Ile Asn Asp Leu Leu Gln Arg Ser

1 5 10 15

Gln Gly Asp Leu Thr Ser Ser Gln His Glu Ile Val His

20 25

SEQ ID NO.4

SEQUENCE LENGTH: 57

SEQUENCE TYPE: amino acid

STRANDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION

Pro Ile Arg Leu Ser Lys Glu Lys Ile Asn Asp Leu Leu Gln Arg Ser

1 5 10 15

Gln Gly Asp Leu Thr Ser Ser Gln His Glu Ile Val His Phe Thr Asp

20 25 30

Val Phe Ile Ala Gly Ser Gly Pro Ile Ser Cys Thr Tyr Ala Arg His

35 40 45

Ile Ile Asp Asn Thr Ser Thr Thr Lys

50 55

SEQ ID NO.5

SEQUENCE LENGTH: 19

SEQUENCE TYPE: amino acid

STRANDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION

Val Tyr Met Ala Glu Ile Gly Ser Gln Asp Asn Pro Val Ile Gly Ala

1 5 10 15

His His Lys

SEQ ID NO.6

SEQUENCE LENGTH: 61

SEQUENCE TYPE: amino acid

STRANDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION

Phe Val Asn Ile Ile Asn Gly Ala Leu Gln Pro Ile Ser Ile Ser Pro

1 5 10 15

Ser Asp Thr Tyr Gln Pro Thr Leu Ala Val Ala Ala Trp Ala Pro Pro

20 25 30

Ile Asp Pro Ala Glu Gly Gln Leu Val Ile Met Gly His Asn Pro Asn

35 40 45

Gln Glu Ala Gly Leu Asn Leu Pro Gly Ser Ala Val Thr

50 55 60

SEQ ID NO.7

SEQUENCE LENGTH: 29

SEQUENCE TYPE: amino acid

STRANDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION

Arg Thr Val Gly Gly Met Ala Thr His Trp Thr Cys Ala Cys Pro Thr

1 5 10 15

Pro His Asp Glu Glu Arg Val Asn Asn Pro Val Asp Lys

20 25

SEQ ID NO.8

SEQUENCE LENGTH: 31

SEQUENCE TYPE: amino acid

STRANDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION

Gln Glu Phe Asp Ala Leu Leu Glu Arg Ala Lys Thr Leu Leu Asn Val

1 5 10 15

His Ser Asp Gln Tyr Asp Asp Ser Ile Arg Gln Ile Val Val Lys

20 25 30

SEQ ID NO.9

SEQUENCE LENGTH: 58

SEQUENCE TYPE: amino acid

STRANDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION

Glu Thr Leu Gln Gln Thr Leu Asp Ala Ser Arg Gly Val Thr Thr Leu

1 5 10 15

Pro Leu Gly Val Glu Arg Arg Thr Asp Asn Pro Ile Tyr Val Thr Trp

20 25 30

Thr Gly Ala Asp Thr Val Leu Gly Asp Val Pro Lys Ser Pro Arg Phe

35 40 45

Ala Leu Val Thr Glu Thr Arg Val Thr Lys

50 55

SEQ ID NO.10

SEQUENCE LENGTH: 30

SEQUENCE TYPE: amino acid

STRANNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION

Leu Ile Val Ser Glu Thr Asn Pro Thr Gln Val Val Ala Ala Leu Leu
1 5 10 15
Arg Asn Leu Asn Thr Ser Asn Asp Glu Leu Val Val Ala Lys
20 25 30

SEQ ID NO.11

SEQUENCE LENGTH: 58

SEQUENCE TYPE: amino acid

STRANNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION

Ser Phe Val Ile Ala Cys Gly Ala Val Cys Thr Pro Gln Ile Leu Trp
1 5 10 15
Asn Ser Asn Ile Arg Pro Tyr Ala Leu Gly Arg Tyr Leu Ser Glu Gln
20 25 30
Ser Met Thr Phe Cys Gln Ile Val Leu Lys Arg Gly Ile Val Asp Ala
35 40 45
Ile Ala Thr Asp Pro Arg Phe Ala Ala Lys
50 55

SEQ ID NO.12

SEQUENCE LENGTH: 51

SEQUENCE TYPE: amino acid

STRANDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION

Val Glu Ala His Lys Lys Lys His Pro Asp Asp Val Leu Pro Ile Pro
1 5 10 15
Phe His Glu Pro Glu Pro Gln Val Met Ile Pro Tyr Thr Ser Asp Phe
20 25 30
Pro Trp His Val Gln Val His Arg Asp Ala Phe Ser Tyr Gly Asp Val
35 40 45
Gly Pro Lys
50

SEQ ID NO.13

SEQUENCE LENGTH: 30

SEQUENCE TYPE: amino acid

STRANDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION

Ala Asp Pro Arg Val Val Val Asp Leu Arg Phe Phe Gly Lys Ser Asp
1 5 10 15
Ile Val Glu Glu Asn Arg Val Thr Phe Gly Pro Asn Pro Lys
20 25 30

SEQ ID NO.14

SEQUENCE LENGTH: 50

SEQUENCE TYPE: amino acid

STRANDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION

Leu Arg Glu Trp Glu Ala Gly Val Thr Asp Thr Tyr Gly Met Pro Gln

1 5 10 15

Pro Thr Phe His Val Lys Arg Thr Asn Ala Asp Gly Asp Arg Asp Gln

20 25 30

Arg Met Met Asn Asp Met Thr Asn Val Ala Asn Met Leu Gly Gly Tyr

30 40 45

Leu Pro

50

SEQ ID NO.15

SEQUENCE LENGTH: 35

SEQUENCE TYPE: amino acid

STRANDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION

Gly Ser Tyr Pro Gln Phe Met Ala Pro Gly Leu Val Leu His Ile Thr

1 5 10 15

Gly Thr Thr Arg Ile Gly Thr Asp Asp Gln Thr Ser Val Ala Asp Pro

20 25 30

Thr Ser Lys

35

SEQ ID NO.16

SEQUENCE LENGTH: 33

SEQUENCE TYPE: amino acid

STRANDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION

Val His Asn Phe Asn Asn Leu Trp Val Gly Gly Asn Gly Cys Ile Pro

1

5

10

15

Asp Ala Thr Ala Cys Asn Pro Thr Arg Thr Ser Val Ala Tyr Ala Leu

20

25

30

Lys

SEQ ID NO.17

SEQUENCE LENGTH: 12

SEQUENCE TYPE: amino acid

STRANDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION

Gly Ala Glu Ala Val Val Asn Tyr Leu Gly Val Ser

1

5

10

SEQ ID NO.18

SEQUENCE LENGTH: 22

SEQUENCE TYPE: amino acid

STRANDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION

Asn Ser Ile Lys Phe Gln Lys Asp Ile Asp Lys Phe Val Asn Ile Ile

1

5

10

15

Asn Gly Ala Leu Gln Pro

20

28

SEQ ID NO.19

SEQUENCE LENGTH: 26

SEQUENCE TYPE: nucleic acid

STRANDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: synthetic DNA

SEQUENCE DESCRIPTION

GAGAGACCAT GGGGTATCGT CTTTCC

26

SEQ ID NO.20

SEQUENCE LENGTH: 27

SEQUENCE TYPE: nucleic acid

STRANDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: synthetic DNA

SEQUENCE DESCRIPTION

GAGAGAGGGAT CCGGAGACGC CAAGGAT

27